

<!--StartFragment-->ALIGNMENTS

```

RESULT 1
Q4W8A9_9CAUL
ID   Q4W8A9_9CAUL               Unreviewed;       257 AA.
AC   Q4W8A9;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   05-FEB-2008, entry version 11.
DE   Carotenoid C2-hydroxylase.
GN   Name=crtG;
OS   Brevundimonas sp. SD212.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC   Caulobacteraceae; Brevundimonas.
OX   NCBI_TaxID=281067;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=SD212;
RX   PubMed=16085816; DOI=10.1128/AEM.71.8.4286-4296.2005;
RA   Nishida Y., Adachi K., Kasai H., Shizuri Y., Shindo K., Sawabe A.,
RA   Komemushi S., Miki W., Misawa N.;
RT   "Elucidation of a carotenoid biosynthesis gene cluster encoding a
RT   novel enzyme, 2,2'-beta-hydroxylase, from Brevundimonas sp. strain
RT   SD212 and combinatorial biosynthesis of new or rare xanthophylls.";
RL   Appl. Environ. Microbiol. 71:4286-4296(2005).
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; AB181388; BAD99415.1; -; Genomic_DNA.
DR   GO; GO:0003824; F:catalytic activity; IEA:InterPro.
DR   GO; GO:0008152; P:metabolic process; IEA:InterPro.
DR   InterPro; IPR006088; Sterol_desatur.
DR   Pfam; PF01598; Sterol_desat; 1.
PE   4: Predicted;
SQ   SEQUENCE   257 AA;  28641 MW;  35F465E7EC8A125C CRC64;

Query Match          100.0%;   Score 1391;   DB 2;   Length 257;
Best Local Similarity 100.0%;   Pred. No. 1.4e-109;
Matches 257;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      1  MLRDLLITTLALSLIIGLRYLLVGAAAHGLLWAGAGRGRLNLRPPAMKRIRAEIVASLI  60
Db      1  MLRDLLITTLALSLIIGLRYLLVGAAAHGLLWAGAGRGRLNLRPPAMKRIRAEIVASLI  60

Qy     61  ACPIYALPAALVLELWKRGGTAIYSDPDAPLWPLVSLIVYLHAHDAFYFVWVHRALHHP  120
Db     61  ACPIYALPAALVLELWKRGGTAIYSDPDAPLWPLVSLIVYLHAHDAFYFVWVHRALHHP  120

Qy    121  RVFGWAHAHEHRSRDPASAFASFAFDPAEAAATAWFLPALALVPIHWGVALTLLTMSLT  180
Db    121  RVFGWAHAHEHRSRDPASAFASFAFDPAEAAATAWFLPALALVPIHWGVALTLLTMSLT  180

Qy    181  AALNHAGREVWPAAWLERAPLRWLITATHHDAHKKRFNGNYGLYFQFQWDRWAGTEVSAAP  240
Db    181  AALNHAGREVWPAAWLERAPLRWLITATHHDAHKKRFNGNYGLYFQFQWDRWAGTEVSAAP  240

Qy    241  SPPSPVIPPERPSAPLR 257
Db    241  SPPSPVIPPERPSAPLR 257

```

RESULT 2

QOGXS3_9CAUL

ID QOGXS3_9CAUL Unreviewed; 257 AA.

AC QOGXS3;

DT 03-OCT-2006, integrated into UniProtKB/TrEMBL.

DT 03-OCT-2006, sequence version 1.

DT 05-FEB-2008, entry version 8.

DE 2,2'-beta-ionone ring hydroxylase.

GN Name=crtG;

OS Brevundimonas aurantiaca.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;

OC Caulobacteraceae; Brevundimonas.

OX NCBI_TaxID=74316;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 15266;

RX PubMed=16781830; DOI=10.1016/j.gene.2006.04.017;

RA Tao L., Rouviere P.E., Cheng Q.;

RT "A carotenoid synthesis gene cluster from a non-marine Brevundimonas

RT that synthesizes hydroxylated astaxanthin.";

RL Gene 379:101-108(2006).

 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

DR EMBL; DQ497427; ABF50965.1; -; Genomic_DNA.

DR GO; GO:0003824; F:catalytic activity; IEA:InterPro.

DR GO; GO:0008152; P:metabolic process; IEA:InterPro.

DR InterPro; IPR006088; Sterol_desatur.

DR Pfam; PF01598; Sterol_desat; 1.

PE 4: Predicted;

SQ SEQUENCE 257 AA; 28653 MW; 5FE010220DF75FE1 CRC64;

Query Match 98.4%; Score 1369; DB 2; Length 257;

Best Local Similarity 98.8%; Pred. No. 1.1e-107;

Matches 254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy      1  MLRDLIITTLALSLIIGLRYLLVGAAAHGLLWAGAGRGALNLRPPAMKRIRAEIVASLI 60
         |||
Db      1  MLRDLIITTLALSLIIGLRYLLVGAAAHGLLWAGAGRGALNLRPPAMKRIRAEIVASLI 60

Qy      61  ACPIYALPAALVLELWKRGGTAIYSDPDANPLWWLPVSLIVYLLAHDAFYVWVHRALHHP 120
         |||
Db      61  ACPIYALPAALVLELWKRGGTAIYSDPDANPLWWLPVSLIVYLLAHDAFYVWVHRALHHP 120

Qy      121 RVFGWAHAHEHRSRDPFAFASFAFDPAEAAATAWFLPALALIVPIHWGVALTLLTMSLT 180
         |||
Db      121 RVFGWAHAHEHRSRDPFAFASFAFDPAEAAATAWFLPALALIVPIHWGVALTLLTMSLT 180

Qy      181 AALNHAGREVWPAAWLERAPLRWLITATHHDAHKKRFNGNYGLYFQFQWDRWAGTEVSAAP 240
         |||
Db      181 AALNHAGREVWPAAWLERAPLRWLITATHHDAHKKRFNGNYGLYFQFQWDRWAGTEVSAAP 240

Qy      241 SPPSPVIPPERPSAPLR 257
         |
Db      241 SRPSPVIPPERPSAPLR 257

```

<!--EndFragment-->